LETTER

REPLY TO PARK ET AL.:

Human ectoparasite transmission of plague during the Second Pandemic is still plausible

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In their letter, Park et al. (1) raise several concerns and question our conclusion (2) that human ectoparasites could have caused plague epidemics during the Second Pandemic.

First, Park et al. (1) state that our study cannot provide evidence that human ectoparasite transmission was more likely than a mixed pneumonic and rat-flea transmission. We have acknowledged this limitation in our discussion, where we wrote that "we did not model mixed transmission routes, and this makes it difficult to fully assess the contribution of pneumonic plague, which commonly occurs during bubonic outbreaks." They assert that this scenario is "highly plausible." We note that while secondary pneumonic infections are common, primary pneumonic transmission through droplets may only occur under particular environmental conditions such as specific temperature or humidity ranges, poor ventilation, and high-density housing (3, 4). For two of the epidemics we used, Moscow and Stockholm, detailed contemporary descriptions of symptoms are available; they indicate bubonic plague with only a few sporadic cases of pneumonic disease (5, 6).

Second, Park et al. (1) criticize the omission of an incubation period in both humans and vectors in all three models and the values of point priors in the human ectoparasite model. Plague can be transmitted by fleas in various ways, not all of which warrant an incubation period (7). Our assumption of early-phase transmission (EPT) is based on current literature stating that EPT provides a better explanation for rapidly spreading epidemics than biofilm-dependent transmission (8). For pneumonic plague, the incubation period is extremely short and it is unlikely that including it in our model would change the fitted dynamics substantially. Furthermore, we demonstrated that the models for pneumonic plague and rat-flea transmission fit well to the outbreaks of known transmission mode during the Third Pandemic, which confirms their individual validity. Point priors used in the human ectoparasite model were largely taken from experimental studies (9, 10). Estimation of all of the parameters in all of the models is problematic due to high parameter correlation, which leads to identifiability problems.

Finally, Park et al. (1) raise an important issue that several technical assumptions such as point priors, uniform priors, and deterministic dynamics may have led to an underestimation of the uncertainty, which could have been better captured using a stochastic model. We agree that the uncertainty in our models could have been larger under different assumptions, which may reduce the possibility of distinguishing between the models based on fit alone. In this situation, we can consider the biological reasonableness of the fitted models. For example, to fit the European mortality curves, the rat-flea model requires a large, highly susceptible rat population and a high transmission rate, which is difficult to justify in Nordic countries (11).

We would like to emphasize that we do not provide evidence against rat-borne plague transmission but explore an alternative explanation of human ectoparasites, which has been suggested by many plague researchers for decades. Our results support our conclusion that human ectoparasites are a plausible and likely vector of plague epidemics during the Second Pandemic. However, we are open to alternative scenarios that could similarly explain the epidemiology of plague in preindustrial Europe under biologically reasonable assumptions.

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